

BLASTP 2.2.15 [Oct-15-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1167230937-26434-74082486310.BLASTQ1

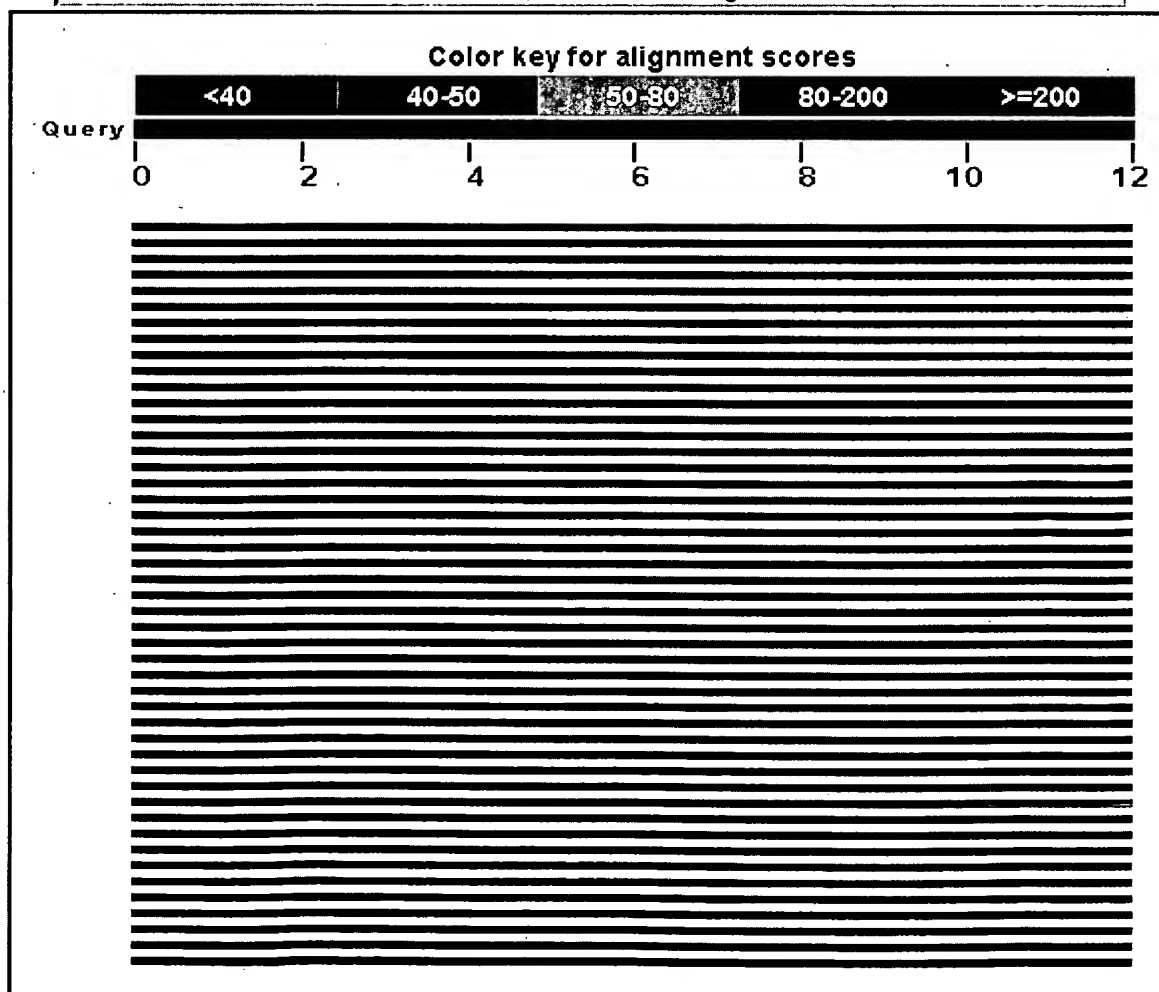
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
4,378,090 sequences; 1,508,613,008 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=12

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments



Distance tree of results ^{NEW}

Sequences producing significant alignments:				Score (Bits)	E Value
gi 114385628 gb ABI74072.1	immunoglobulin light chain variable			40.1	0.013
gi 114385652 gb ABI74084.1	immunoglobulin light chain variab...			40.1	0.013
gi 114385610 gb ABI74063.1	immunoglobulin light chain variable			40.1	0.013
gi 114385612 gb ABI74064.1	immunoglobulin light chain variable			40.1	0.013
gi 114385618 gb ABI74067.1	immunoglobulin light chain variable			40.1	0.013
gi 109693236 gb ABG38407.1	immunoglobulin light chain variable			40.1	0.013
gi 109693204 gb ABG38393.1	immunoglobulin light chain variable			40.1	0.013
gi 109693202 gb ABG38392.1	immunoglobulin light chain variable			40.1	0.013
gi 109693140 gb ABG38363.1	immunoglobulin light chain variable			40.1	0.013
gi 109104332 ref XP_001096602.1	PREDICTED: similar to Ig kap...			40.1	0.013 G
gi 109104329 ref XP_001096027.1	PREDICTED: similar to Ig kap...			40.1	0.013 G
gi 98956320 emb CAI99798.1	immunoglobulin kappa light chain var			40.1	0.013
gi 98956427 emb CAI99852.1	immunoglobulin kappa light chain var			40.1	0.013
gi 98956314 emb CAI99795.1	immunoglobulin kappa light chain var			40.1	0.013
gi 98956248 emb CAI99762.1	immunoglobulin kappa light chain var			40.1	0.013
gi 98956278 emb CAI99777.1	immunoglobulin kappa light chain var			40.1	0.013
gi 98956206 emb CAI99740.1	immunoglobulin kappa light chain var			40.1	0.013
gi 77378238 gb ABA70841.1	immunoglobulin kappa light chain vari			40.1	0.013
gi 77379554 gb ABA71431.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 77379548 gb ABA71429.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 77378240 gb ABA70842.1	immunoglobulin kappa light chain vari			40.1	0.013
gi 77378351 gb ABA70890.1	immunoglobulin kappa light chain vari			40.1	0.013
gi 77379428 gb ABA71371.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 77379556 gb ABA71432.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 62822265 gb AA114814.1	unknown [Homo sapiens]			40.1	0.013
gi 40748164 gb AAR89568.1	immunoglobulin light chain variable r			40.1	0.013
gi 40748180 gb AAR89576.1	immunoglobulin light chain variable r			40.1	0.013
gi 40748182 gb AAR89577.1	immunoglobulin light chain variable r			40.1	0.013
gi 37728236 gb AAO45455.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 37693760 gb AAQ98891.1	immunoglobulin kappa light chain v...			40.1	0.013
gi 33570192 gb AAQ21993.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570006 gb AAQ21904.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570835 gb AAQ22305.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570849 gb AAQ22312.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570483 gb AAQ22134.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570487 gb AAQ22136.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570501 gb AAQ22142.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570498 gb AAQ22141.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570196 gb AAQ21995.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570514 gb AAQ22147.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570518 gb AAQ22149.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570190 gb AAQ21992.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570504 gb AAQ22143.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570847 gb AAQ22311.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570206 gb AAQ22000.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570008 gb AAQ21905.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570216 gb AAQ22004.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570012 gb AAQ21907.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 33570208 gb AAQ22001.1	immunoglobulin kappa chain variable r			40.1	0.013
gi 4323828 gb AAD16553.1	immunoglobulin kappa light chain varia			40.1	0.013 U

<u>gi 21706664 gb AAH34142.1 </u>	IGKV1-5 protein [Homo sapiens]	<u>40.1</u>	0.013	UG
<u>gi 2072272 gb AAB61657.1 </u>	immunoglobulin rearranged light chain	<u>40.1</u>	0.013	G
<u>gi 6110578 gb AAF03884.1 AF184767.1</u>	Ig kappa chain [Homo sapiens]	<u>40.1</u>	0.013	
<u>gi 15919720 gb AAL10927.1 </u>	immunoglobulin kappa chain variable r	<u>40.1</u>	0.013	
<u>gi 15919727 gb AAL10930.1 </u>	immunoglobulin kappa chain variable r	<u>40.1</u>	0.013	
<u>gi 18307302 gb AAL65722.1 </u>	immunoglobulin light chain kappa vari	<u>40.1</u>	0.013	
<u>gi 17980196 gb AAL50552.1 AF377321.1</u>	recombinant single chain...	<u>40.1</u>	0.013	
<u>gi 21311289 gb AAM46643.1 </u>	immunoglobulin kappa light chain [Hom	<u>40.1</u>	0.013	G
<u>gi 21310994 gb AAM46497.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 21310876 gb AAM46440.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 4323960 gb AAD16619.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	
<u>gi 4323874 gb AAD16576.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	
<u>gi 18025604 gb AAK94811.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 21310698 gb AAM46352.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 4324004 gb AAD16641.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	
<u>gi 21311327 gb AAM46662.1 </u>	anti-pneumococcal antibody A7 ligh...	<u>40.1</u>	0.013	
<u>gi 21310897 gb AAM46450.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 15637431 gb AAL04523.1 AF408725.1</u>	anti-pneumococcal capsul...	<u>40.1</u>	0.013	G
<u>gi 21310899 gb AAM46451.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 15919729 gb AAL10931.1 </u>	immunoglobulin kappa chain variable r	<u>40.1</u>	0.013	
<u>gi 4323886 gb AAD16582.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	G
<u>gi 15919717 gb AAL10926.1 </u>	immunoglobulin kappa chain variable r	<u>40.1</u>	0.013	
<u>gi 21311072 gb AAM46535.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 21310850 gb AAM46427.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 642379 gb AAA61844.1 </u>	immunoglobulin kappa-chain	<u>40.1</u>	0.013	
<u>gi 8777871 gb AAF79132.1 </u>	immunoglobulin light chain variable re	<u>40.1</u>	0.013	
<u>gi 4323890 gb AAD16584.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	
<u>gi 22086576 gb AAM90680.1 AF402942.1</u>	thyroid peroxidase autoa...	<u>40.1</u>	0.013	G
<u>gi 21310777 gb AAM46391.1 </u>	immunoglobulin kappa light chain v...	<u>40.1</u>	0.013	
<u>gi 21311064 gb AAM46531.1 </u>	immunoglobulin kappa light chain vari	<u>40.1</u>	0.013	
<u>gi 18092624 gb AAL59381.1 </u>	anti-cardiolipin immunoglobulin light	<u>40.1</u>	0.013	
<u>gi 397796 gb AAA20108.1 </u>	immunoglobulin kappa chain	<u>40.1</u>	0.013	
<u>gi 4323816 gb AAD16547.1 </u>	immunoglobulin kappa light chain varia	<u>40.1</u>	0.013	
<u>gi 8777885 gb AAF79139.1 </u>	immunoglobulin light chain variable re	<u>40.1</u>	0.013	
<u>gi 619760 gb AAA60341.1 </u>	immunoglobulin kappa light chain V regi	<u>40.1</u>	0.013	
<u>gi 84798170 gb ABC67034.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 84798168 gb ABC67033.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 84798176 gb ABC67037.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 84798172 gb ABC67035.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 84797930 gb ABC66914.1 </u>	immunoglobulin light chain variabl...	<u>40.1</u>	0.013	
<u>gi 81020120 gb ABB55180.1 </u>	immunoglobulin kappa light chain v...	<u>40.1</u>	0.013	
<u>gi 75707459 gb ABA26193.1 </u>	immunoglobulin light chain variable r	<u>40.1</u>	0.013	
<u>gi 75707455 gb ABA26191.1 </u>	immunoglobulin light chain variable r	<u>40.1</u>	0.013	
<u>gi 75707445 gb ABA26186.1 </u>	immunoglobulin light chain variable r	<u>40.1</u>	0.013	
<u>gi 5578780 emb CAB51290.1 </u>	immunoglobulin kappa chain variable r	<u>40.1</u>	0.013	G
<u>gi 16076189 emb CAC94321.1 </u>	immunoglobulin kappa chain variable	<u>40.1</u>	0.013	
<u>gi 12655714 emb CAC27673.1 </u>	immunoglobulin kappa chain variable	<u>40.1</u>	0.013	
<u>gi 16116887 emb CAC94621.1 </u>	immunoglobulin kappa chain variable	<u>40.1</u>	0.013	
<u>gi 1335175 emb CAA31202.1 </u>	immunoglobulin kappa light chain [Hom	<u>40.1</u>	0.013	G
<u>gi 10637404 emb CAC10873.1 </u>	immunoglobulin kappa chain variable	<u>40.1</u>	0.013	G

Alignments

Get selected sequences

Select all

Deselect all

Distance tree of results

> gi|114385628|gb|ABI74072.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|114385652|gb|ABI74084.1| immunoglobulin light chain variable region [Homo sapiens]
gi|114385654|gb|ABI74085.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|114385610|gb|ABI74063.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|114385612|gb|ABI74064.1| immunoglobulin light chain variable region [Homo sapiens]
Length=111

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|114385618|gb|ABI74067.1| immunoglobulin light chain variable region [Homo sapiens]
Length=114

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|109693236|gb|ABG38407.1| immunoglobulin light chain variable region [Homo sapiens]
Length=114

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 26 37

> gi|109693204|gb|ABG38393.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|109693202|gb|ABG38392.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|109693140|gb|ABG38363.1| immunoglobulin light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 24 35

> gi|109104332|ref|XP_001096602.1| **G** PREDICTED: similar to Ig kappa chain V-II region GM607 p1
[Macaca mulatta]
Length=184

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 44 55

> gi|109104329|ref|XP_001096027.1| **G** PREDICTED: similar to Ig kappa chain V-II region GM607 p1
[Macaca mulatta]
Length=148

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 44 55

> gi|98956320|emb|CAI99798.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=108

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHSNGY 12
Sbjct 21 32

> gi|98956427|emb|CAI99852.1| immunoglobulin kappa light chain variable region [Homo sapiens]

Length=110 ..

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 22 33

> gi|98956314|emb|CAI99795.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=92

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|98956248|emb|CAI99762.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=114

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|98956278|emb|CAI99777.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=111

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|98956206|emb|CAI99740.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=112

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|77378238|qb|ABA70841.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=121

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|77379554|qb|ABA71431.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=109

Score = 40.1 bits (87), Expect = 0.013

Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 13 24

> gi|77379548|gb|ABA71429.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=109

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 13 24

> gi|77378240|gb|ABA70842.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=121

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 24 35

> gi|77378351|gb|ABA70890.1| immunoglobulin kappa light chain variable region [Homo sapiens]
Length=100

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 5 16

> gi|77379428|gb|ABA71371.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=121

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 24 35

> gi|77379556|gb|ABA71432.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=108

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12
Sbjct 13 24

> gi|62822265|gb|AAY14814.1| unknown [Homo sapiens]
Length=121

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLHSNGY 12

Sbjct 44 55

> gi|40748164|gb|AAR89568.1| immunoglobulin light chain variable region [Homo sapiens]
Length=87

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 5 16

> gi|40748180|gb|AAR89576.1| immunoglobulin light chain variable region [Homo sapiens]
Length=86

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 5 16

> gi|40748182|gb|AAR89577.1| immunoglobulin light chain variable region [Homo sapiens]
Length=84

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 4 15

> gi|37728236|gb|AAO45455.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=100

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|37693760|gb|AAQ98891.1| immunoglobulin kappa light chain variable region [synthetic const]
Length=112

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 24 35

> gi|33570192|gb|AAQ21993.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=95

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLHLSNGY 12
Sbjct 17 28

> gi|33570006|gb|AAQ21904.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=96

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570835|gb|AAQ22305.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=92

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570849|gb|AAQ22312.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=97

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570483|gb|AAQ22134.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570487|gb|AAQ22136.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=97

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570501|gb|AAQ22142.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=91

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570498|gb|AAQ22141.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=92

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570196|gb|AAQ21995.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570514|gb|AAQ22147.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=92

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570518|gb|AAQ22149.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=97

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570190|gb|AAQ21992.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=93

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570504|gb|AAQ22143.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=93

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570847|gb|AAQ22311.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570206|gb|AAQ22000.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=93

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 14 25

> gi|33570008|gb|AAQ21905.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=96

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 17 28

> gi|33570216|gb|AAQ22004.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 20 31

> gi|33570012|gb|AAQ21907.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|33570208|gb|AAQ22001.1| immunoglobulin kappa chain variable region [Homo sapiens]
Length=98

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 19 30

> gi|4323828|gb|AAD16553.1| **U** immunoglobulin kappa light chain variable region [Homo sapiens]
Length=101

Score = 40.1 bits (87), Expect = 0.013
Identities = 12/12 (100%), Positives = 12/12 (100%), Gaps = 0/12 (0%)

Query 1 RSSQSLLSNGY 12
Sbjct 16 27

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Dec 26, 2006 5:53 PM

Number of letters in database: 1,508,613,008

Number of sequences in database: 4,378,090

Lambda K H
0.349 0.278 1.70

Gapped
Lambda K H
0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 4378090

Number of Hits to DB: 12696356

Number of extensions: 173938

Number of successful extensions: 659

Number of sequences better than 20000: 658

Number of HSP's better than 20000 without gapping: 0

Number of HSP's gapped: 659

Number of HSP's successfully gapped: 659

Length of query: 12

Length of database: 1508613008

Length adjustment: 2

Effective length of query: 10

Effective length of database: 1499856828

Effective search space: 14998568280

Effective search space used: 14998568280

T: 11

A: 40

X1: 14 (7.0 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 39 (19.7 bits)

S2: 39 (19.7 bits)

All Databases

PubMed

Nucleotide

Protein

Genome

Structure

OMIM

PMC

Journals

Books

Search for

☒ Limits ☐ Preview/Index ☐ History ☐ Clipboard ☐ Details

Field: Title/Abstract

- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

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Most Recent Queries

Time Result

#35 Related Articles for PubMed (Select 10231096)	16:36:30	148
#34 Related Articles for PubMed (Select 14523945)	16:30:24	624
#29 Related Articles for PubMed (Select 9114042)	16:30:04	377
#31 Search #29 AND (HTLV* or "T-cell leukemia" or "T-cell lymphotropic") Field: Title/Abstract	16:29:09	6
#28 Search (antibod* or immunoglob*) AND (MHC or "histocompatibility complex" or TCR-like or "T-cell receptor like") AND (peptide or antigen or epitope) Field: Title/Abstract	16:08:56	4507
#30 Search #29 AND #27	16:08:49	3
#27 Search REiter[au] AND "peptide-specific"[ti]	16:08:34	4

Write to the Help Desk

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Dec 18 2006 06:34:27

WEST Search History

DATE: Wednesday, December 27, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L21	L18 not(l19 or L8)	100
<input type="checkbox"/>	L20	L18 (not l19 or L8)	34673749
<input type="checkbox"/>	L19	L18 and l16	28
<input type="checkbox"/>	L18	L17 and l14	129
<input type="checkbox"/>	L17	L9 and (exotoxin adj A or exotoxin near3 Pseudomonas)	376
<input type="checkbox"/>	L16	l12 and antibod\$ with (peptide antigen or epitope) near5 (HLA adj A2 or MHC-I or class adj I near3 (MHC or histocompatibility))	100
<input type="checkbox"/>	L15	l12 and antibod\$ same (peptide antigen or epitope) near5 (HLA adj A2 or MHC-I or class adj I near3 (MHC or histocompatibility))	184
<input type="checkbox"/>	L14	l12 and (HLA adj A2 or MHC-I or class adj I near3 (MHC or histocompatibility))	362
<input type="checkbox"/>	L13	L12 and l4	392
<input type="checkbox"/>	L12	L11 and l10	392
<input type="checkbox"/>	L11	L9 and complex near5 (MHC\$2 or histocompatibility adj complex or antigen adj presenting or HLA\$3) near3 (peptide or antigen or epitope)	1150
<input type="checkbox"/>	L10	L9 and l7	664
<input type="checkbox"/>	L9	(antibod\$ or immunoglob\$) with (bind\$4 or specific\$5 or recogniz\$5 or target\$5) with (MHC\$2 or histocompatibility adj complex or antigen adj presenting or HLA\$3) near5 (peptide or antigen or epitope)	2356
<input type="checkbox"/>	L8	L7 and antibod\$ same (TCR or T adj cell adj receptor) adj like	14
<input type="checkbox"/>	L7	L6 and l5	1253
<input type="checkbox"/>	L6	L4 and l2	1903
<input type="checkbox"/>	L5	L3 and (HTLV-1 or (t-cell adj (leukemia or lymphotropic) adj virus) or retrovir\$5)	1789
<input type="checkbox"/>	L4	L1 and (epitope or peptide or antigen) with (\$viral or \$virus)	2615
<input type="checkbox"/>	L3	L1 and (epitope or peptide or antigen) same (\$viral or \$virus)	3089
<input type="checkbox"/>	L2	L1 and (antibod\$ or immunoglob\$) same (toxin or cytotoxi\$5 or exotoxin)	2751
<input type="checkbox"/>	L1	(antibod\$ or immunoglob\$) same (bind\$4 or specific\$5 or recogniz\$5 or target\$5) with (MHC\$2 or histocompatibility adj complex or antigen adj presenting or HLA\$3) near5 (peptide or antigen or epitope)	4263

END OF SEARCH HISTORY